

## Exhibit 2: Alignment of Xenopus APC (Query) with Human APC (Subject)

```

> gb|AAA60353.1| UG polyposis locus-encoded protein
Length=2844

Score = 1360 bits (3520), Expect = 0.0, Method: Composition-based stats.
Identities = 747/861 (86%), Positives = 797/861 (92%), Gaps = 6/861 (0%)

Query 1 MAAASYDQLVKQVEALTMENLNLRQLEEDNSNHLTKLETEATNMKEVLKQLQGSIEDEAM 60
Sbjct 1 MAAASYDQLVKQVEALTMENLNLRQLEEDNSNHLTKLETEATNMKEVLKQLQGSIEDEAM 60

Query 61 ASSGPIDLLERFKDLNLDSSNIPAGKARPKMSRYSYGSREGSLSGHSGECSPVPVGSFQR 120
Sbjct 61 ASSGPIDLLERFKDLNLDSSNIPAGKARPKMSRYSYGSREGSVSSRSGECSPVPVGSFPR 120

Query 121 RGLNGSRESAGYMEELEKERLLIAEHEKEEKEKRWYQAQLQNLTKRIDSPLTENFSM 180
Sbjct 121 RGFVNGSRESAGYMEELEKERLLIAEHEKEEKEKRWYQAQLQNLTKRIDSPLTENFSL 180

Query 181 QDTMTRRQLEYEARQIRAAEMEEQLGTCQDMEKRVQTRVGKIHQIEEILIRQLLQSQVA 240
Sbjct 181 QDTLRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQIEKDILIRQLLQSQAT 240

Query 241 EAAERTPQSKHDAGSRDAEKLDPGQGTSEITASGNVSGQGSSSRADHDTTSMSSNSTY 300
Sbjct 241 EA-ERSSQNKHETGSHDAERQNEQGVGEINMATS-GNGQGSTTRMDHETASVLSSTSH 298

Query 301 SVPRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCI+MRQSGCLPLLIQ 360
Sbjct 299 SAPRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCIMRQSGCLPLLIQ 358

Query 361 LLHGNDKDSVLLGNSRGSKEARASGAALNDNIHSQPDCKRGRREIRVLHLEQIRAYCE 420
Sbjct 359 LLHGNDKDSVLLGNSRGSKEARASGAALNDNIHSQPDCKRGRREIRVLHLEQIRAYCE 418

Query 421 TCWEWQEAHEQGMDQDKNMPAPVDHQICPAVCLVMKLSFDEEHRHAMNELGGQLQAI AEL 480
Sbjct 419 TCWEWQEAHEPGMDQDKNMPAPVEHQICPAVCLVMKLSFDEEHRHAMNELGGQLQAI AEL 478

Query 481 LQVDCMYGLINDHYSVTLRRYAGMALTNLTFGVDVANKATLCSMKSCMRALVAQLKSESE 540
Sbjct 479 LQVDCMYGLINDHYSITLRRYAGMALTNLTFGVDVANKATLCSMKGCMRALVAQLKSESE 538

Query 541 DLQQVIASVLRNLNLSWRADVNSKKTLEVGSVKALMECALDVKKESTLKSVLASALWNLSAH 600
Sbjct 539 DLQQVIASVLRNLNLSWRADVNSKKTLEVGSVKALMECALDVKKESTLKSVLASALWNLSAH 598

Query 601 CTENKADICSDGALAFVLVSTLTYSRQTNTLAIIESGGGILRNVSLLIATNEDHRQILRE 660
Sbjct 599 CTENKADICAVDGALAFVLVGTLTYSRQTNTLAIIESGGGILRNVSLLIATNEDHRQILRE 658

```

Query	661	NNCLQTLQLKSHSLTIVSNACGTLWNLSARNAKDQEBGLWDMGAVSMLKNLIHSHKHKMI	720
		NNCLQTLQLKSHSLTIVSNACGTLWNLSARN KDQE LWDMGAVSMLKNLIHSHKHKMI	
Sbjct	659	NNCLQTLQLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHSHKHKMI	718
Query	721	AMGSAAALRNLMANRPAPYKDANIMSPGSSVPSLHVRKQKALEAELDAQHLSETFDNIDN	780
		AMGSAAALRNLMANRPAPYKDANIMSPGSS+PSLHVRKQKALEAELDAQHLSETFDNIDN	
Sbjct	719	AMGSAAALRNLMANRPAPYKDANIMSPGSSLP SLHVRKQKALEAELDAQHLSETFDNIDN	778
Query	781	LSPKTTTHRNKQRHKQNLCSLEYALDSSRHDDSI CRSDNFSIGNLTVLSPYINTTVLPGSSS	840
		LSPK +HR+KQRHKQ+L +Y D++RHDD+ RSDNF+ GN+TVLSPY+NTTVLP SSS	
Sbjct	779	LSPKASHRSKQRHKQSLYGDYVFD TNRHDDN - -RSDNFNTGNMTVLSPYLNTTVLPSSSS	836
Query	841	PRPTMDGSRPEKDR--ERTAG	859
		R ++D SR EKDR ER G	
Sbjct	837	SRGSLDSSRSEKDRSLERER G	857